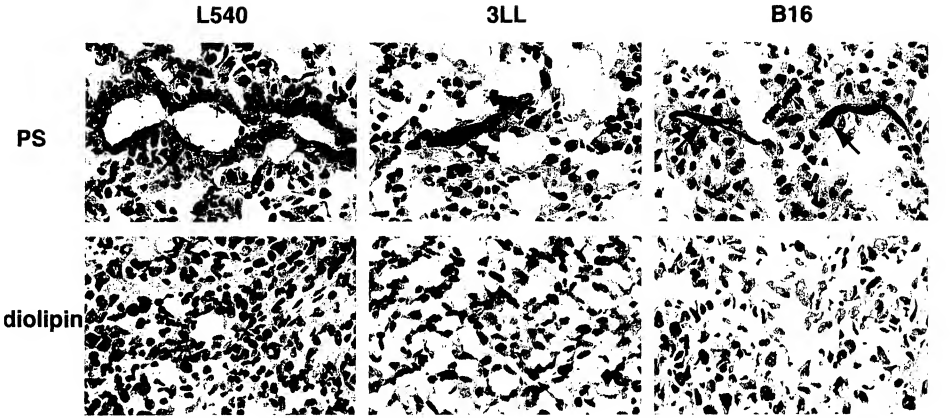


FIG. 1

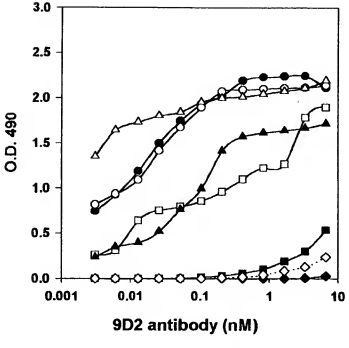

3.0
2.5
2.0
1.5
1.0
0.5
0.0
O.D. 490
0.001
0.01
0.1
1
10
9D2 antibody (nM)

FIG. 2A

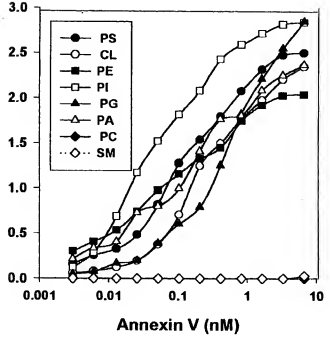

PS
CL
PE
PI
PG
PA
PC
SM
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0.001
0.01
0.1
1
10
Annexin V (nM)

FIG. 2B

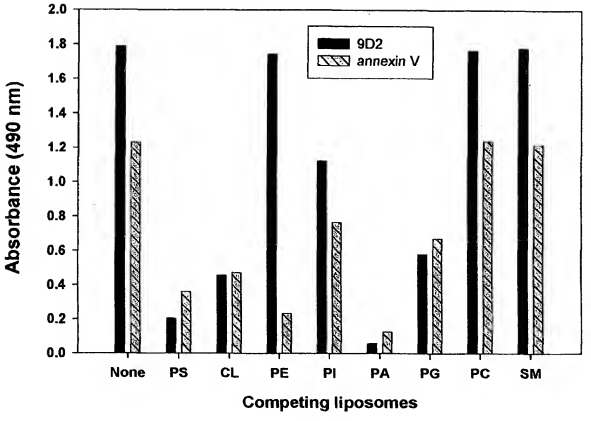

2.0
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Absorbance (490 nm)
9D2
annexin V
None
PS
CL
PE
PI
PA
PG
PC
SM
Competing liposomes

FIG. 3

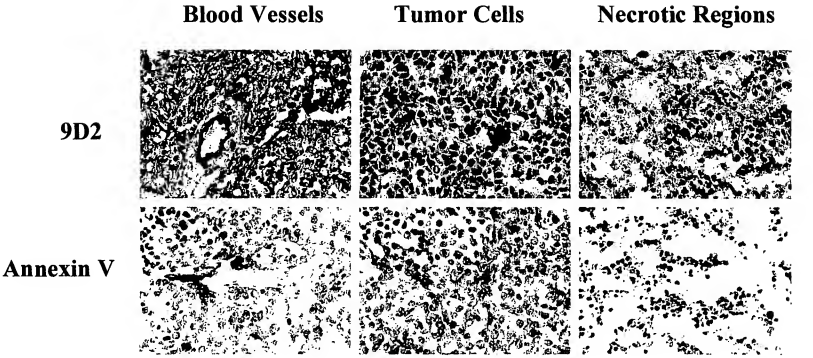


FIG. 4

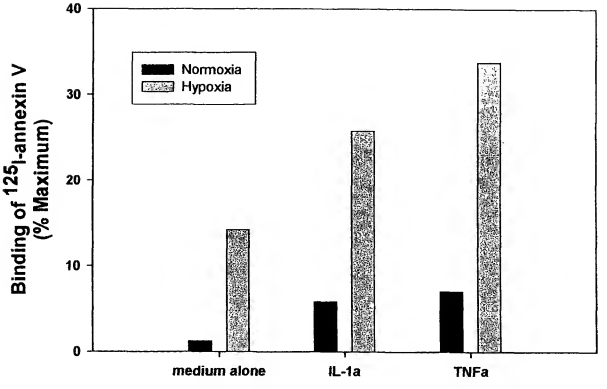

Binding of 125I-annexin V
(% Maximum)
40
30
20
10
0
Normoxia
Hypoxia
medium alone
IL-1a
TNFa

FIG. 5

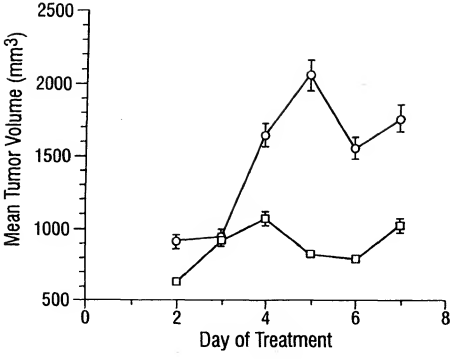

2500
2000
1500
1000
500
Mean Tumor Volume (mm3)
0
2
4
6
8
Day of Treatment

FIG. 6A

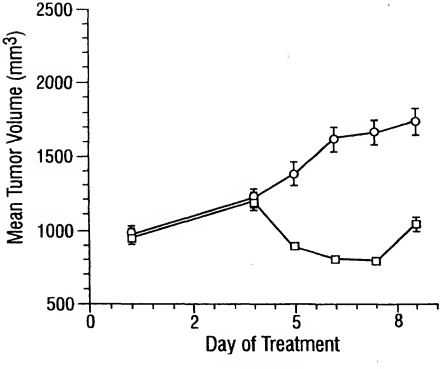

2500
2000
1500
1000
500
Mean Tumor Volume (mm3)
0
2
5
8
Day of Treatment

FIG. 6B

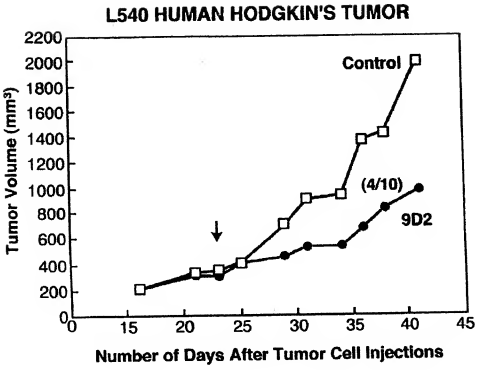

L540 HUMAN HODGKIN'S TUMOR
Tumor Volume (mm³)
2200
2000
1800
1600
1400
1200
1000
800
600
400
200
0
0
15
20
25
30
35
40
45
Number of Days After Tumor Cell Injections
Control
(4/10)
9D2

FIG. 7

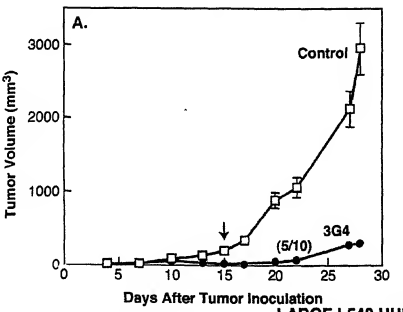


FIG. 8A

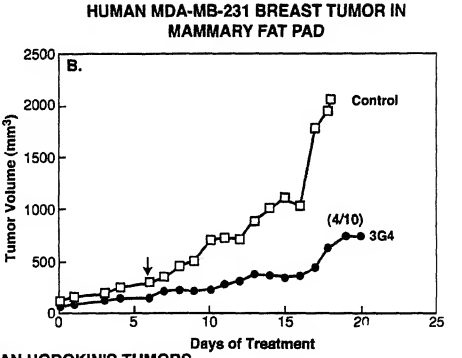


FIG. 8B

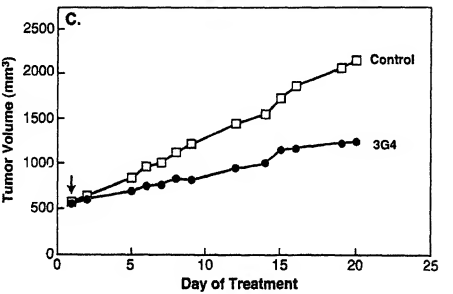


FIG. 8C

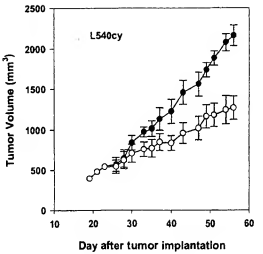


FIG. 8D

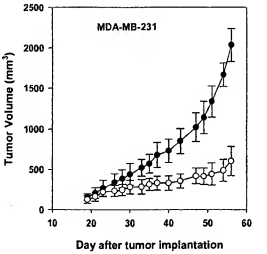


FIG. 8E

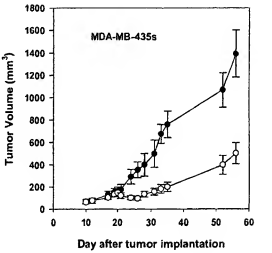


FIG. 8F

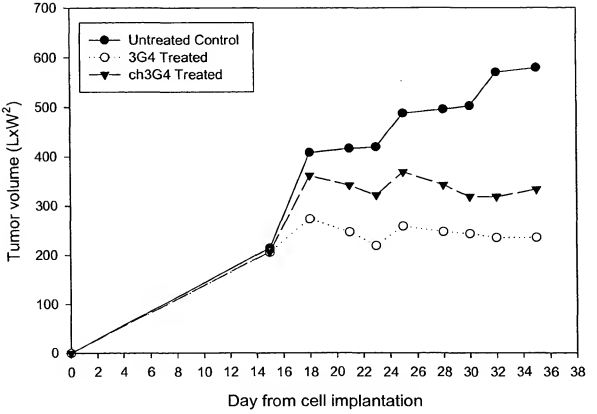

Untreated Control
3G4 Treated
ch3G4 Treated
Tumor volume (LxW2)
Day from cell implantation
0
100
200
300
400
500
600
700
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38

FIG. 8G

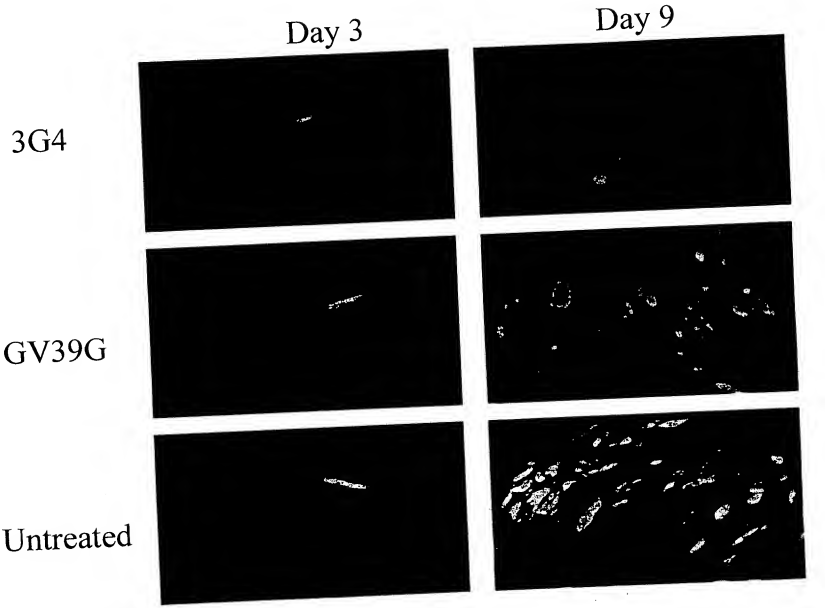


FIG. 9A

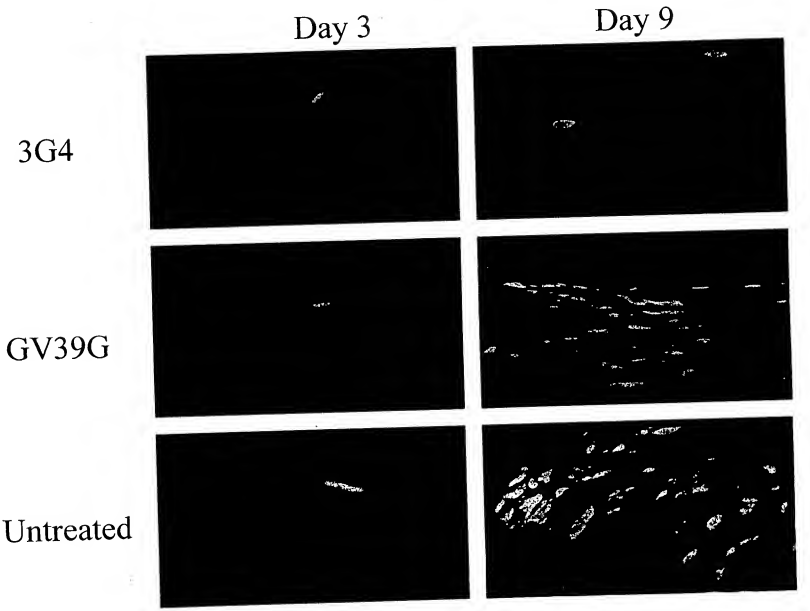


FIG. 9B

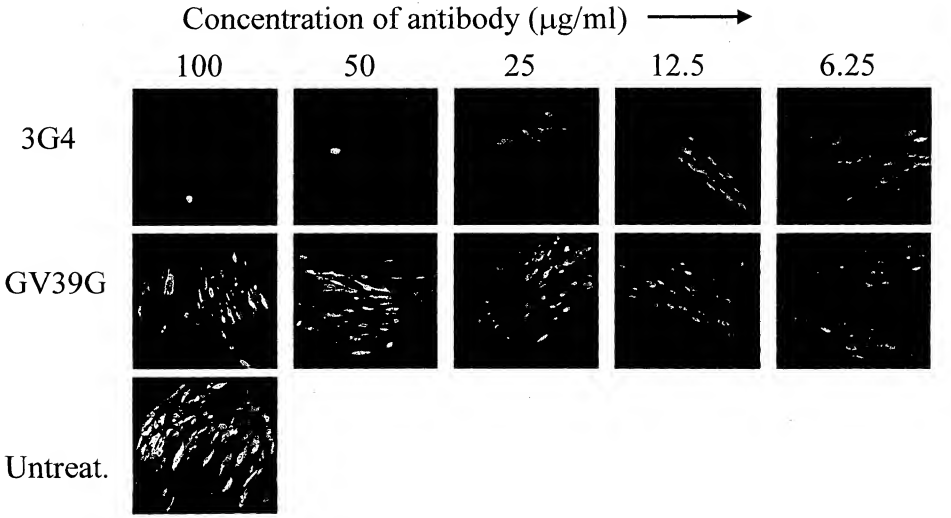

Concentration of antibody (μg/ml)
100
50
25
12.5
6.25
3G4
GV39G
Untreat.

FIG. 10

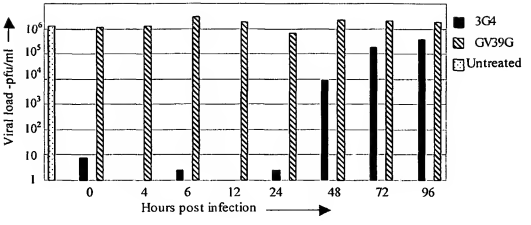

Viral load -pfu/ml
10^6
10^5
10^4
10^3
10^2
10
1
0
4
6
12
24
48
72
96
Hours post infection
3G4
GV39G
Untreated

FIG. 11C

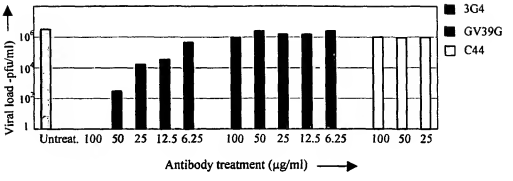


FIG. 11A

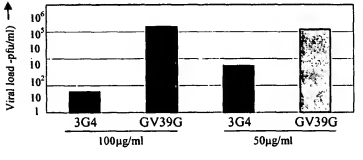


FIG. 11B

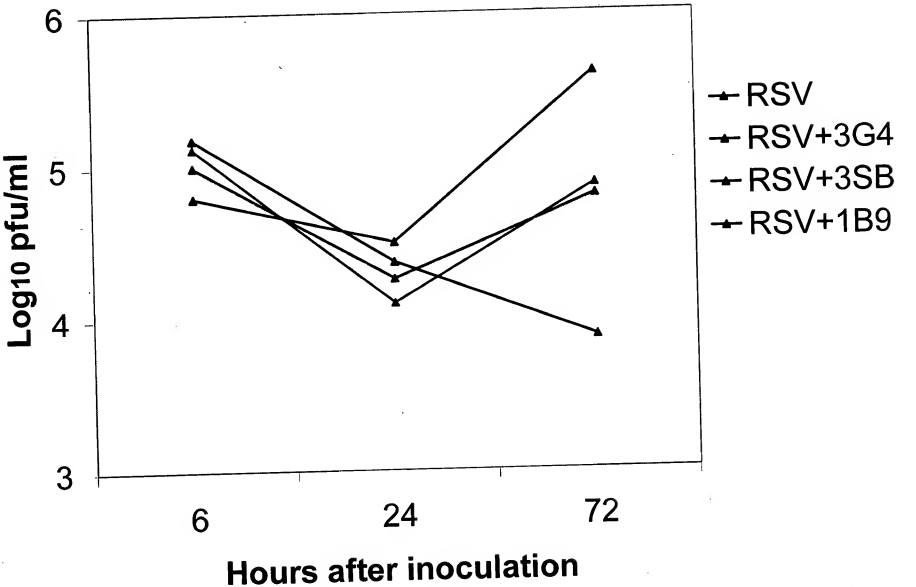

6
5
4
3
Log10 pfu/ml
6
24
72
Hours after inoculation
RSV
RSV+3G4
RSV+3SB
RSV+1B9

FIG. 12

FIG. 13A. DLB

FIG. 13B. DIB

FIG. 13C. $(DLB)_4NA$

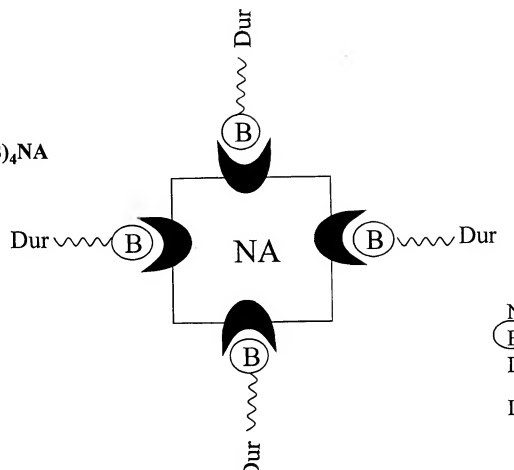
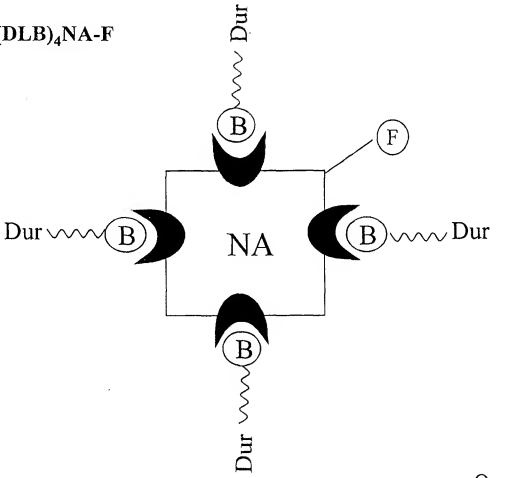


FIG. 13D. $(DLB)_4NA$-F

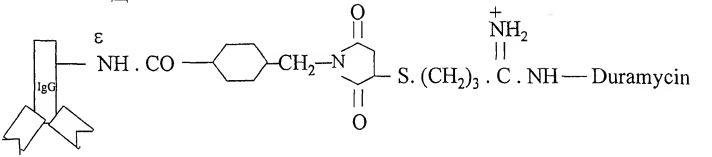


NA = neutravidin
(B) = biotin
Dur = Duramycin

Dur ~~~ (B) = DLB

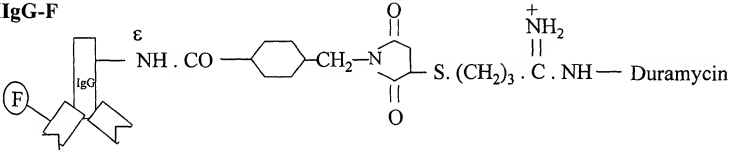
(F) = fluorescein

FIG. 13E. $(DIM)_n$ HIgG



n = 5 to 8 Duramycin residues per IgG
Monomer (150,000 Da) is shown

FIG. 13F. $(DIM)_n$ HIgG-F

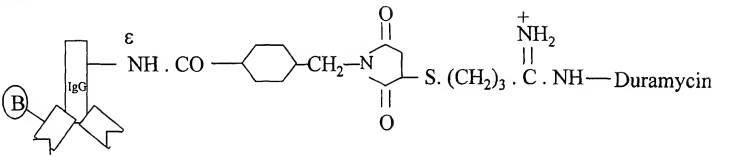


n = 5 to 8 Duramycin residues per IgG

(F) = fluorescein

Monomer (150,000 Da) is shown

FIG. 13G. $(DIM)_n$ HIgG-B

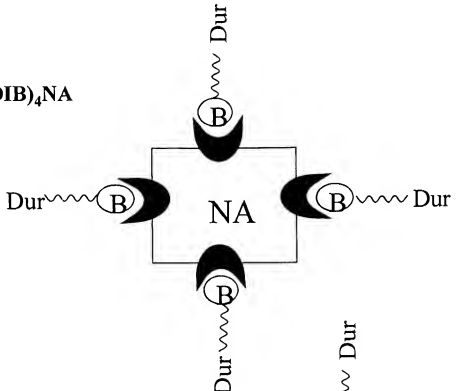


n = 5 to 8 Duramycin residues per IgG

(B) = biotin

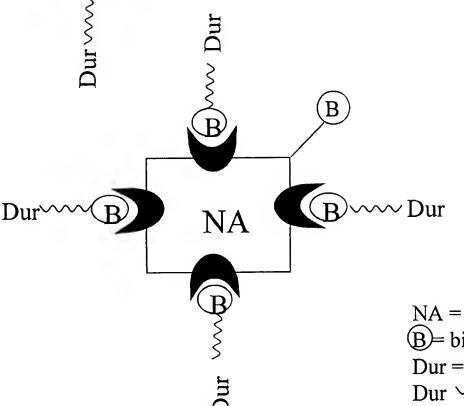
Monomer (150,000 Da) is shown

FIG. 13H. $(DIB)_4NA$



NA = neutravidin
B = biotin
Dur = Duramycin
Dur ~~~ B = DIB

FIG. 13I. $(DIB)_4NA\text{-}B$



NA = neutravidin
B = biotin
Dur = Duramycin
Dur ~~~ B = DIB

FIG. 13J. DS-1

FIG. 13K. DS-2

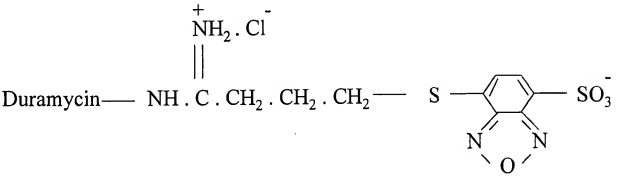


FIG. 13L. DS-3

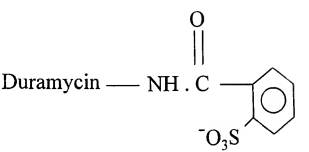


FIG. 13M. DS-4

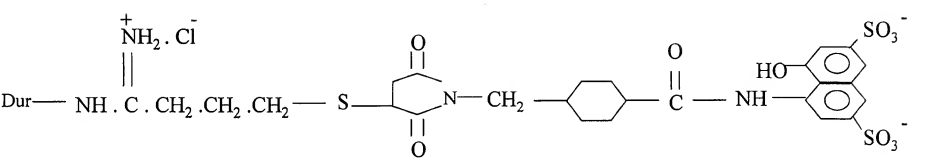
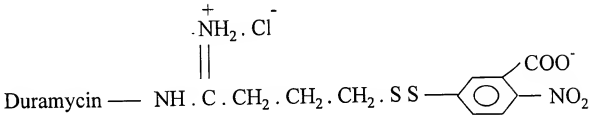


FIG. 13N. DS-5

FIG. 13O. DC-1



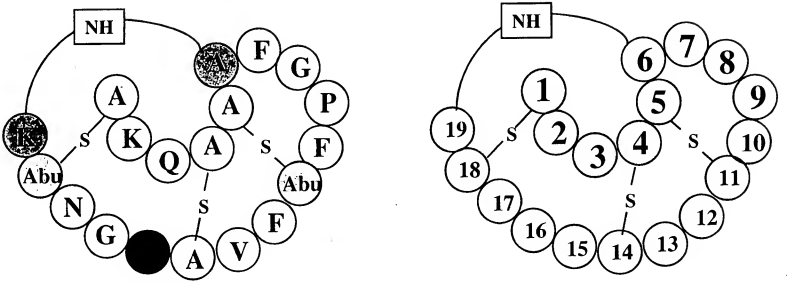
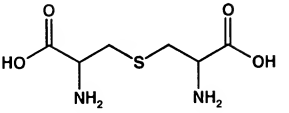
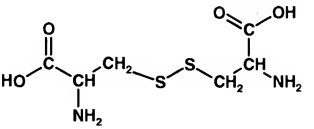

NH
F
G
A
A
P
K
Q
A
F
Abu
Abu
N
G
A
V
F
S
S
S
NH
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
S
S
S

FIG. 13P

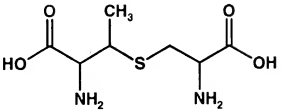


Lanthionine

Ala-S-Ala

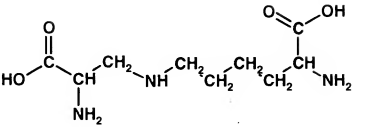


cystine



β-methyllanthionine

Abu-S-Ala

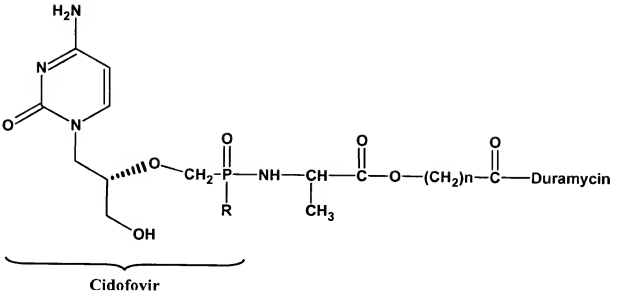


Lysinoalanine

Ala-NH-Lys

FIG. 13Q

FIG. 13R



R= OH, as in cidofovir, or labile hydrophobic group

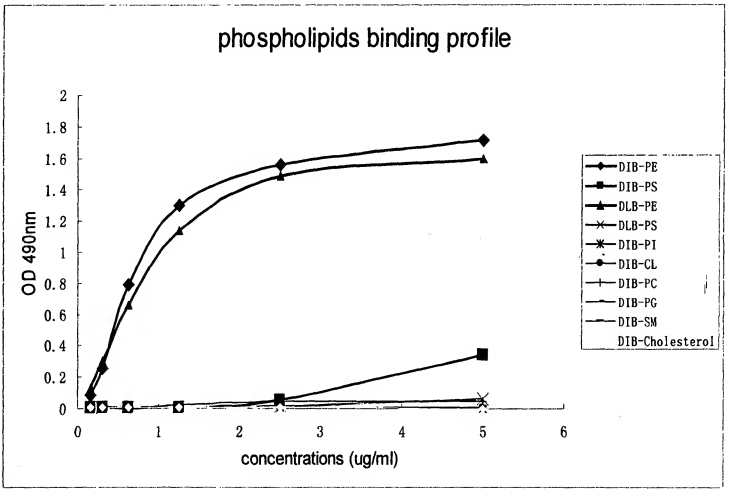

phospholipids binding profile
OD 490nm
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
1
2
3
4
5
6
concentrations (ug/ml)
DIB-PE
DIB-PS
DLB-PE
DLB-PS
DIB-PI
DIB-CL
DIB-PC
DIB-PG
DIB-SM
DIB-Cholesterol

FIG. 14A

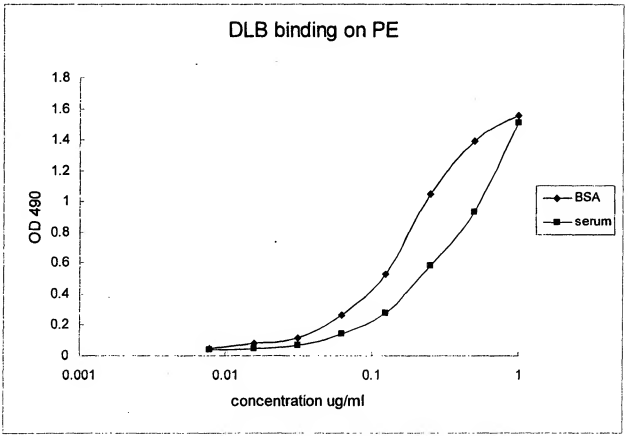

DLB binding on PE
OD 490
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
concentration ug/ml
BSA
serum

FIG. 14B

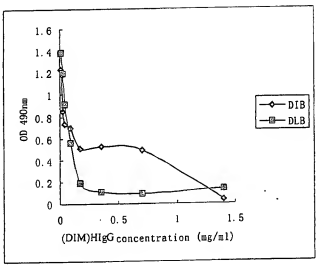


FIG. 14C

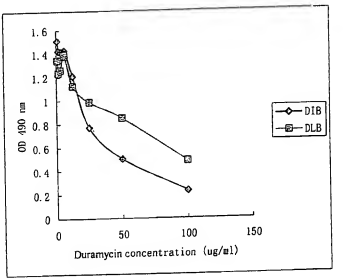


FIG. 14D

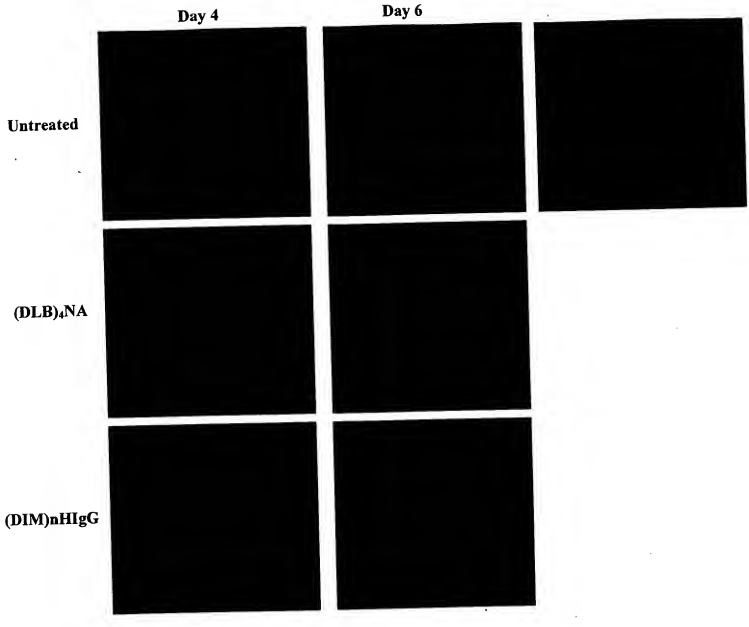


FIG. 15

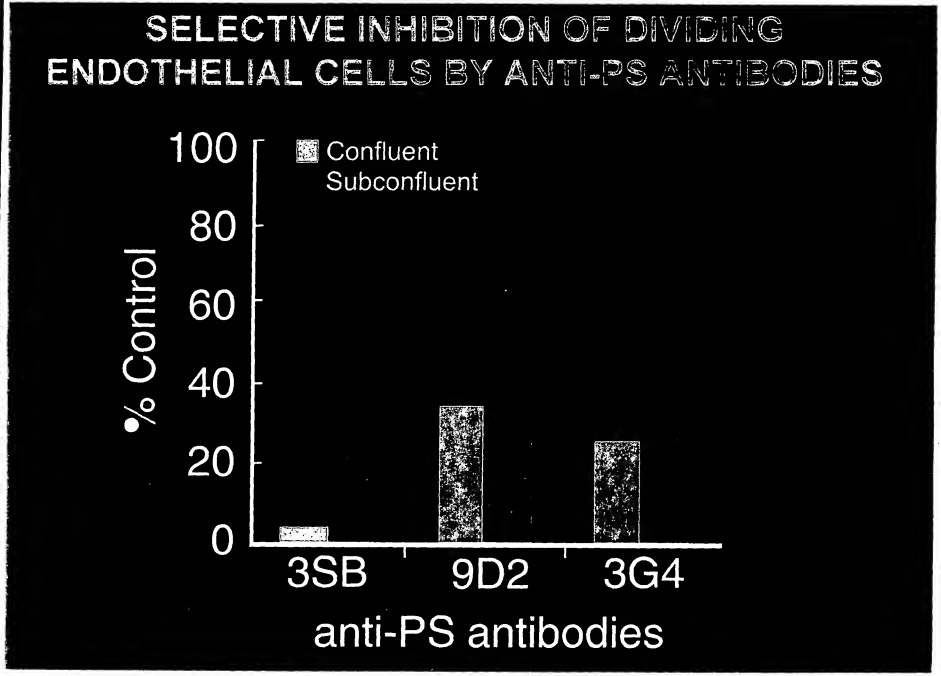

SELECTIVE INHIBITION OF DIVIDING ENDOTHELIAL CELLS BY ANTI-PS ANTIBODIES
100
80
60
40
20
0
% Control
Confluent
Subconfluent
3SB
9D2
3G4
anti-PS antibodies

FIG. 16

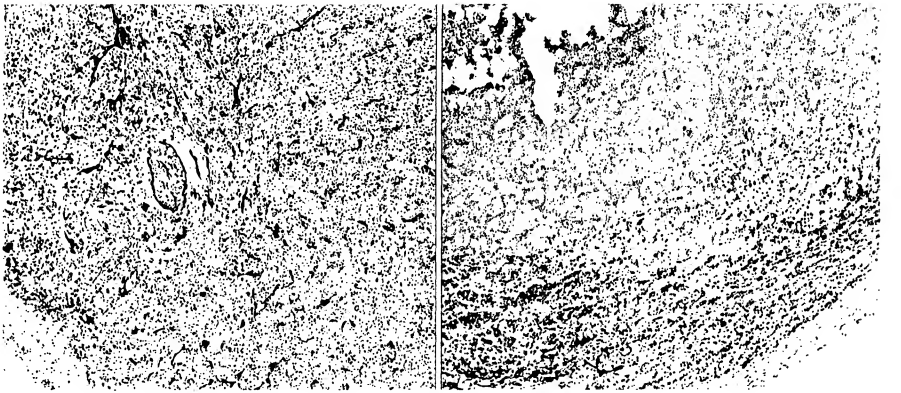


FIG. 17A

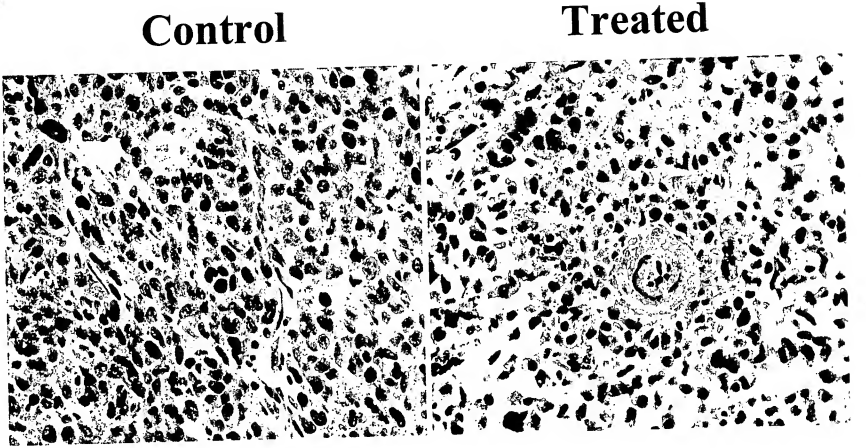


FIG. 17B

FIG. 18A

3G4-2BVH original sequence:

```
                                        M   G   W   T   W   I   F   I   L   I   L   S   V
121                                     ATG GGA TGG ACC TGG ATC TTT ATT TTA ATC CTG TCA GTA
                                        TAC CCT ACC TGG ACC TAG AAA TAA AAT TAG GAC AGT CAT
                                            PvuII
                                            ~~~~~~~
         T   T   G   V   H   S   E   V   Q   L   Q   Q   S   G   P   E   L   E   K   P
181      ACT ACA GGT GTC CAC TCT GAG GTC CAG CTG CAG CAG TCT GGA CCT GAG CTG GAG AAG CCT
         TGA TGT CCA CAG GTG AGA CTC CAG GTC GAC GTC GTC AGA CCT GGA CTC GAC CTC TTC GGA
          G   A   S   V   K   L   S   C   K   A   S   G   Y   S   F   T   G   Y   N   M
241      GGC GCT TCA GTG AAG CTA TCC TGC AAG GCT TCT GGT TAC TCA TTC ACT GGC TAC AAC ATG
         CCG CGA AGT CAC TTC GAT AGG ACG TTC CGA AGA CCA ATG AGT AAG TGA CCG ATG TTG TAC
          N   W   V   K   Q   S   H   G   K   S   L   E   W   I   G   H   I   D   P   Y
301      AAC TGG GTG AAA CAG AGC CAT GGA AAG AGC CTT GAA TGG ATT GGA CAT ATT GAT CCT TAC
         TTG ACC CAC TTT GTC TCG GTA CCT TTC TCG GAA CTT ACC TAA CCT GTA TAA CTA GGA ATG
           Y   G   D   T   S   Y   N   Q   K   F   R   G   K   A   T   L   T   V   D   K
361      TAT GGT GAT ACT TCC TAC AAC CAG AAG TTC AGG GGC AAG GCC ACA TTG ACT GTA GAC AAA
         ATA CCA CTA TGA AGG ATG TTG GTC TTC AAG TCC CCG TTC CGG TGT AAC TGA CAT CTG TTT
           S   S   S   T   A   Y   M   Q   L   K   S   L   T   S   E   D   S   A   V   Y
421      TCC TCC AGC ACA GCC TAC ATG CAG CTC AAG AGC CTG ACA TCT GAG GAC TCT GCA GTC TAT
         AGG AGG TCG TGT CGG ATG TAC GTC GAG TTC TCG GAC TGT AGA CTC CTG AGA CGT CAG ATA
           Y   C   V   K   G   G   Y   Y   G   H   W   Y   F   D   V   W   G   A   G   T
481      TAC TGT GTA AAG GGG GGT TAC TAC GGG CAC TGG TAC TTC GAT GTC TGG GGC GCA GGG ACC
         ATG ACA CAT TTC CCC CCA ATG ATG CCC GTG ACC ATG AAG CTA CAG ACC CCG CGT CCC TGG
           BstEII
           ~~~~~~~~~
         T   V   T   V   S   S   A   T   T   T   A   P   S   V   Y   P   L   V   P
541      ACG GTC ACC GTC TCC TCA GCT ACA ACA ACA GCC CCA TCT GTC TAT CCC TTG GTC CCG GGC
         TGC CAG TGG CAG AGG AGT CGA TGT TGT TGT CGG GGT AGA CAG ATA GGG AAC CAG GGC CCG
         BamHI                   EcoRI                                   XhoI
         ~~~~~~~~                ~~~~~~~~                                ~~~~~~~~
601      GGA TCC CCC GGG CTG CAG GAA TTC GAT ATC AAG CTT ATC GAT ACC GTC GAC CTC GAG GGG
         CCT AGG GGG CCC GAC GTC CTT AAG CTA TAG TTC GAA TAG CTA TGG CAG CTG GAG CTC CCC
```

The RACE product 3G4-2BVH is cloned and grafted onto the human γ1 constant region at the BstEII site. Thus, it contains the mouse leader sequence and its VH is joined with the human CH1 sequence in the following way: leader/3G4VH/VSS-AST…

```
         Mouse Leader              ↓mature protein
   1  MGWTWIFILI LSVTTGVHSE VQLQQSGPEL EKPGASVKLS CKASGYSFTG
  51  YNMNWVKQSH GKSLEWIGHI DPYYGDTSYN QKFRGKATLT VDKSSSTAYM
                                                ↓BstEII graft site
 101  QLKSLTSEDS AVYYCVKGGY YGHWYFDVWG AGTTVTVSS ASTKGPSVFPL
 151  APSSKSTSG                                   ↑human γ1CH1
```

FIG. 18B

3G4-2BVL original sequence:

```
                                                                  M   D   M   R   A
  61                                                             ATG GAC ATG AGG GCT
                                                                 TAC CTG TAC TCC CGA
       P   A   Q   I   L   G   F   L   L   L   L   F   P   G   T   R   C   D   I   Q
 121   CCT GCA CAG ATT TTG GGC TTC TTG TTG CTC TTG TTT CCA GGT ACC AGA TGT GAC ATC CAG
       GGA CGT GTC TAA AAC CCG AAG AAC AAC GAG AAC AAA GGT CCA TGG TCT ACA CTG TAG GTC
       M   T   Q   S   P   S   S   L   S   A   S   L   G   E   R   V   S   L   T   C
 181   ATG ACC CAG TCT CCA TCC TCC TTA TCT GCC TCT CTG GGA GAA AGA GTC AGT CTC ACT TGT
       TAC TGG GTC AGA GGT AGG AGG AAT AGA CGG AGA GAC CCT CTT TCT CAG TCA GAG TGA ACA
       R   A   S   Q   D   I   G   S   S   L   N   W   L   Q   Q   G   P   D   G   T
 241   CGG GCA AGT CAG GAC ATT GGT AGT AGC TTA AAC TGG CTT CAG CAG GGA CCA GAT GGA ACT
       GCC CGT TCA GTC CTG TAA CCA TCA TCG AAT TTG ACC GAA GTC GTC CCT GGT CTA CCT TGA
       I   K   R   L   I   Y   A   T   S   S   L   D   S   G   V   P   K   R   F   S
 301   ATT AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GAT TCT GGT GTC CCC AAA AGG TTC AGT
       TAA TTT GCG GAC TAG ATG CGG TGT AGG TCA AAT CTA AGA CCA CAG GGG TTT TCC AAG TCA
       G   S   R   S   G   S   D   Y   S   L   T   I   S   S   L   E   S   E   D   F
 361   GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC AGC CTT GAG TCT GAA GAT TTT
       CCG TCA TCC AGA CCC AGT CTA ATA AGA GAG TGG TAG TCG TCG GAA CTC AGA CTT CTA AAA
       V   D   Y   Y   C   L   Q   Y   V   S   S   P   P   T   F   G   A   G   T   K
 421   GTA GAC TAT TAC TGT CTA CAA TAT GTT AGT TCT CCT CCC ACG TTC GGT GCT GGG ACC AAG
       CAT CTG ATA ATG ACA GAT GTT ATA CAA TCA AGA GGA GGG TGC AAG CCA CGA CCC TGG TTC
                                                 BbsI                BamHI
                                                 ~~~~~~              ~~~~~~
       L   E   L   K   R   A   D   A   A   P   T   V   F   I   F   G   R   I   P
 481   CTG GAG CTG AAA CGG GCT GAT GCT GCA CCA ACT GTC TTC ATC TTC GGG CGG ATC CCC CGG
       GAC CTC GAC TTT GCC CGA CTA CGA CGT GGT TGA CAG AAG TAG AAG CCC GCC TAG GGG GCC
```

The RACE product 3G4-2BVL is grafted to human κ constant region at the BbsI site. Thus, it contains the mouse leader sequence and its VL is joined withIN the human CL1 sequence in the following way: leader/3G4-VL/TVF-IFP…

```
          Mouse Leader              ↓mature protein
   1  MDMRAPAQIL GFLLLLFPGT RCDIQMTQSP SSLSASLGER VSLTCRASQD
  51  IGSSLNWLQQ GPDGTIKRLI YATSSLDSGV PKRFSGSRSG SDYSLTISSL
                                    FR4↓          ↓BbsI graft site
 101  ESEDFVDYYC LQYVSSPPTF GAGTKLELKR ADAAPTVF IFPPSDEQLKSGTAS
                                                 ↑ human kappa constant
```

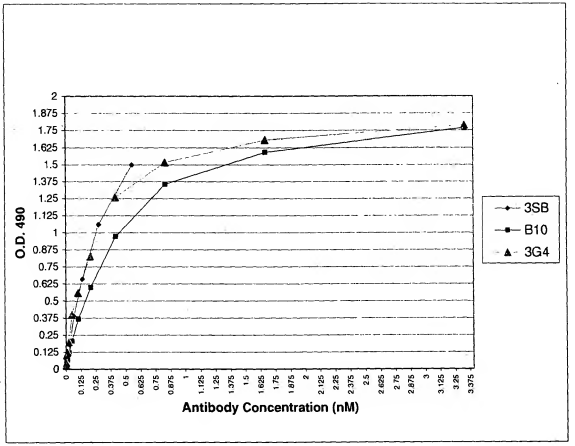

O.D. 490
2
1.875
1.75
1.625
1.5
1.375
1.25
1.125
1
0.875
0.75
0.625
0.5
0.375
0.25
0.125
0
0 0.125 0.25 0.375 0.5 0.625 0.75 0.875 1 1.125 1.25 1.375 1.5 1.625 1.75 1.875 2 2.125 2.25 2.375 2.5 2.625 2.75 2.875 3 3.125 3.25 3.375
Antibody Concentration (nM)
3SB
B10
3G4

FIG. 19A

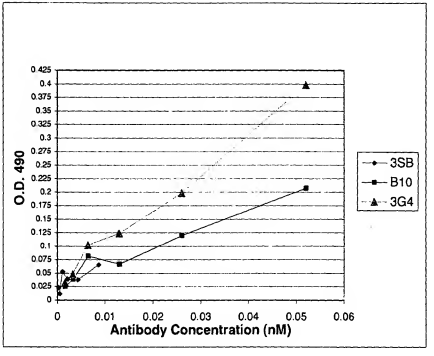

O.D. 490
0.425
0.4
0.375
0.35
0.325
0.3
0.275
0.25
0.225
0.2
0.175
0.15
0.125
0.1
0.075
0.05
0.025
0
0
0.01
0.02
0.03
0.04
0.05
0.06
Antibody Concentration (nM)
3SB
B10
3G4

FIG. 19B

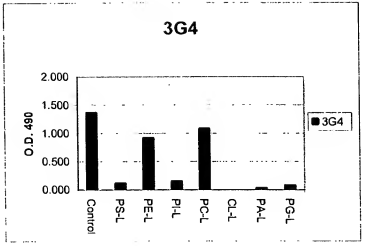

3G4
2.000
1.500
1.000
0.500
0.000
O.D. 490
3G4
Control
PS-L
PE-L
PI-L
PC-L
CL-L
PA-L
PG-L

FIG. 20

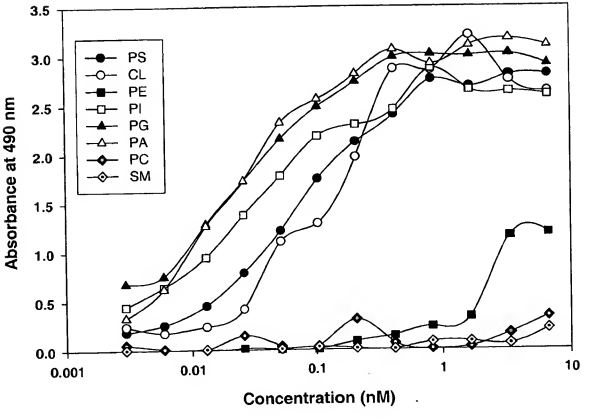

3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Absorbance at 490 nm
PS
CL
PE
PI
PG
PA
PC
SM
0.001
0.01
0.1
1
10
Concentration (nM)

FIG. 21

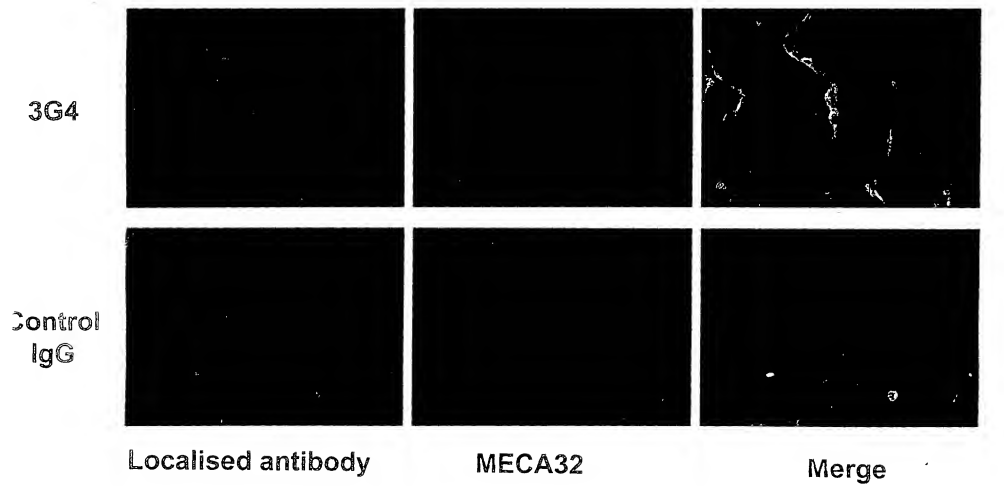

LOCALIZATION OF ch3G4 TO BLOOD VESSELS IN
ORTHOTOPIC MDA-MB-435 TUMORS IN MICE
3G4
Control IgG
Localised antibody
MECA32
Merge

FIG. 22

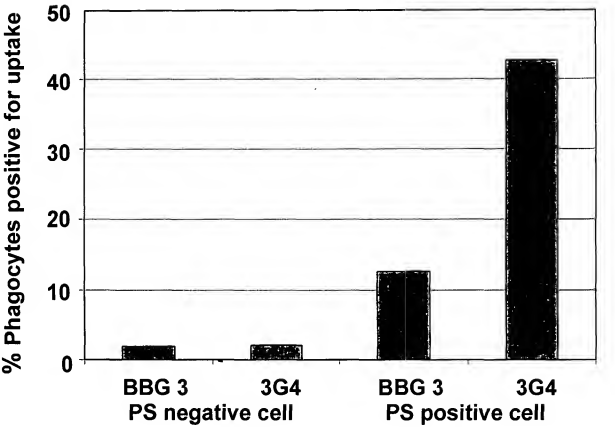

% Phagocytes positive for uptake
50
40
30
20
10
0
BBG 3
3G4
PS negative cell
BBG 3
3G4
PS positive cell

FIG. 23

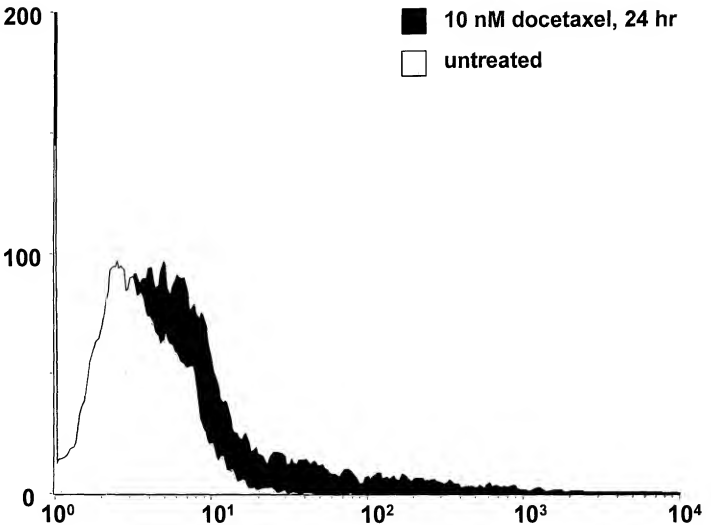

HUVEC
200
100
0
10 nM docetaxel, 24 hr
untreated
10^0
10^1
10^2
10^3
10^4

FIG. 24A

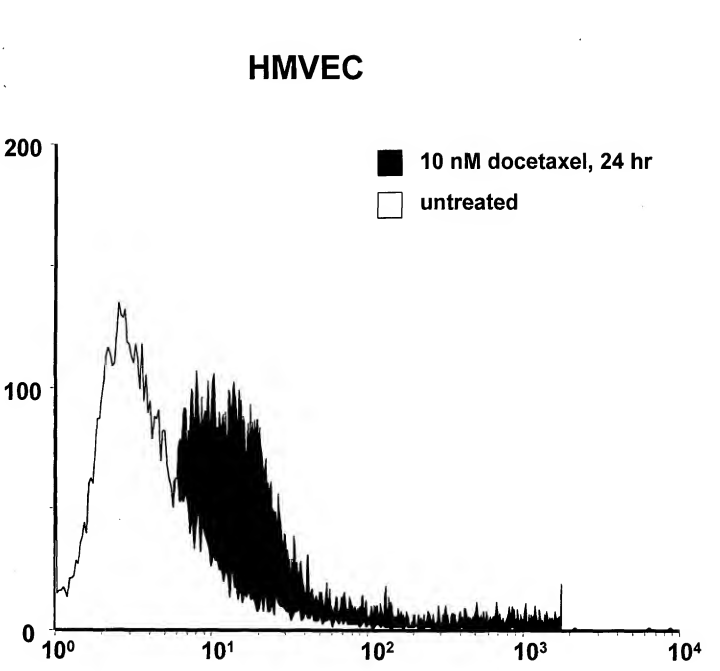

HMVEC
200
100
0
10 nM docetaxel, 24 hr
untreated
10^0
10^1
10^2
10^3
10^4

FIG. 24B

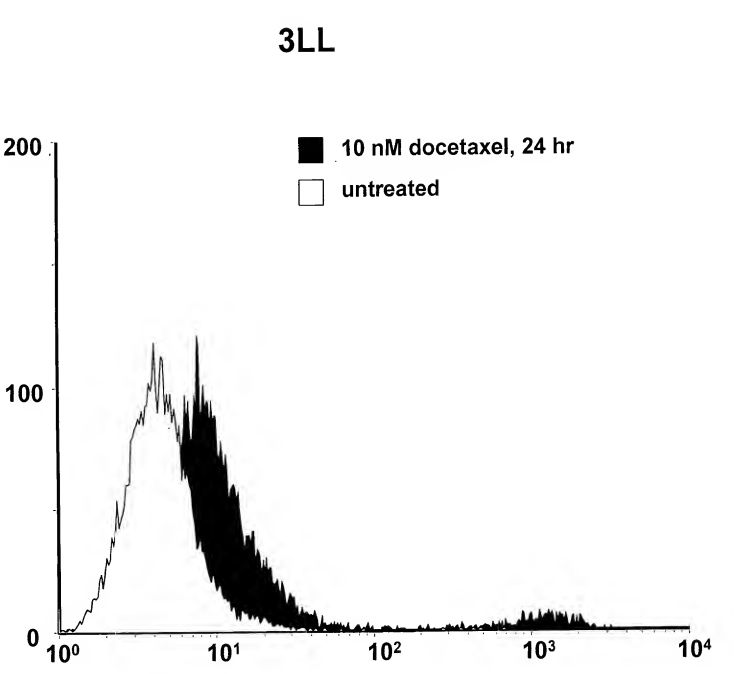

3LL
200
100
0
10 nM docetaxel, 24 hr
untreated
10⁰
10¹
10²
10³
10⁴

FIG. 25A

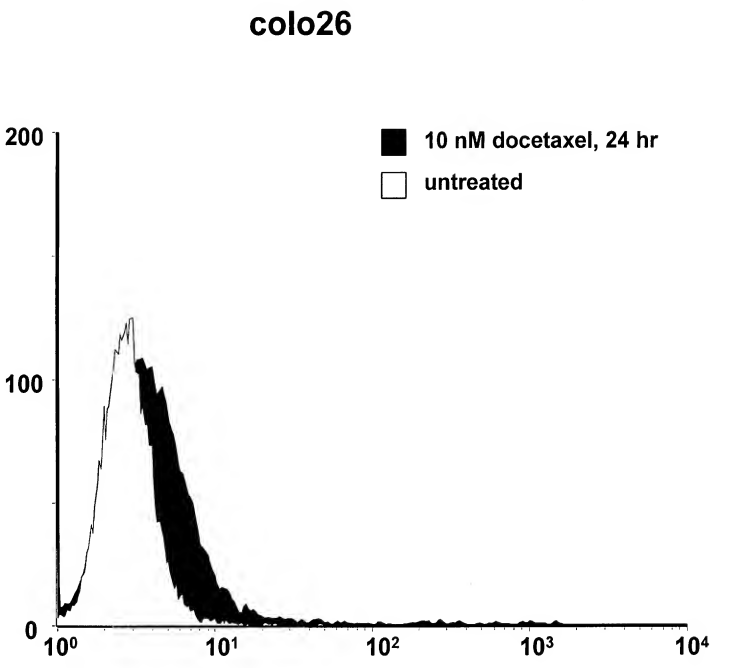

colo26
200
100
0
10 nM docetaxel, 24 hr
untreated
10^0
10^1
10^2
10^3
10^4

FIG. 25B

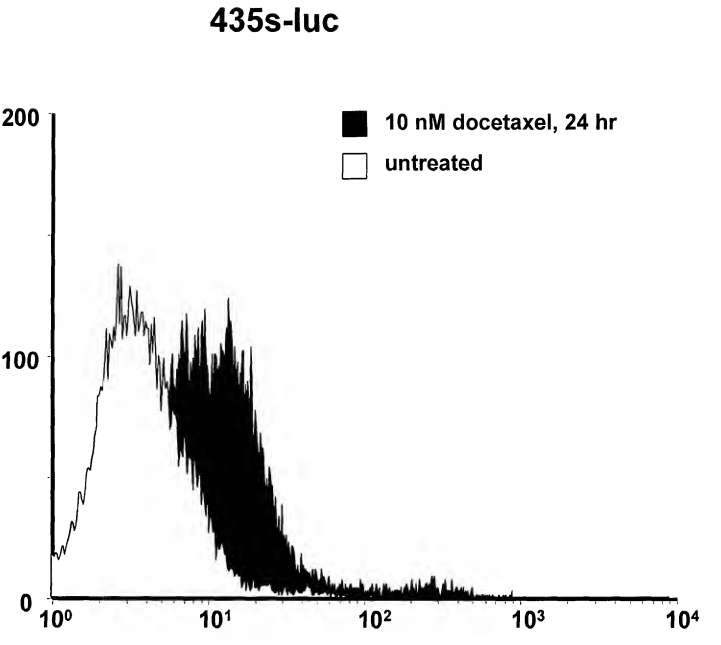

435s-luc
200
100
0
10 nM docetaxel, 24 hr
untreated
10⁰
10¹
10²
10³
10⁴

FIG. 25C

Binding of 3G4 to MDA-MB-231 to by FACS

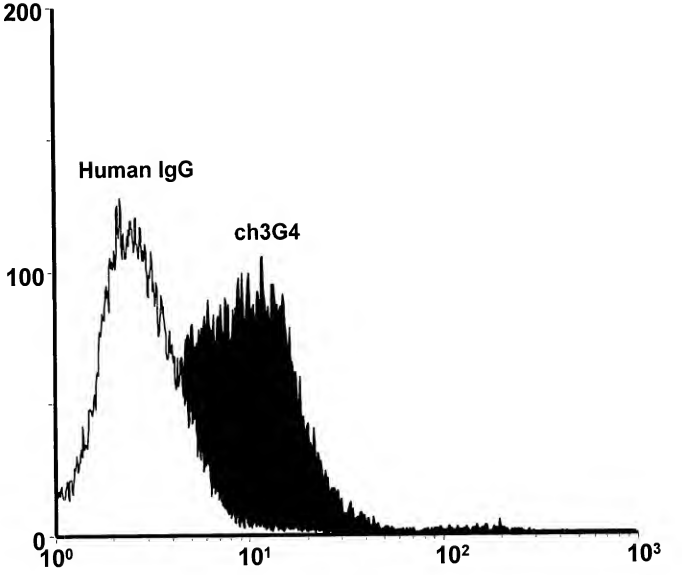


FIG. 26

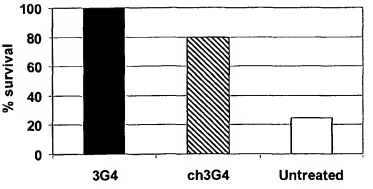


FIG. 27

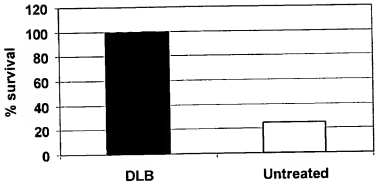


FIG. 28

FIG. 29A

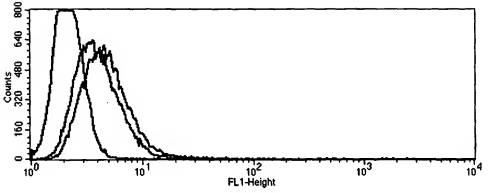
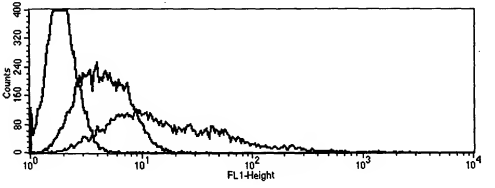


FIG. 29B



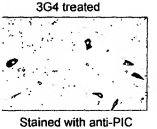


FIG. 30A

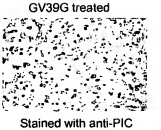


FIG. 30B

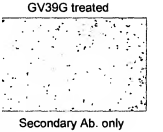


FIG. 30C

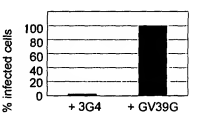


FIG. 30D

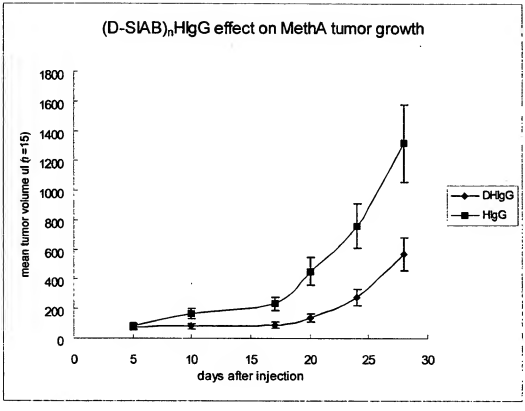

(D-SIAB)nHIgG effect on MethA tumor growth
mean tumor volume ul (n=15)
1800
1600
1400
1200
1000
800
600
400
200
0
0
5
10
15
20
25
30
days after injection
DHIgG
HIgG

FIG. 31

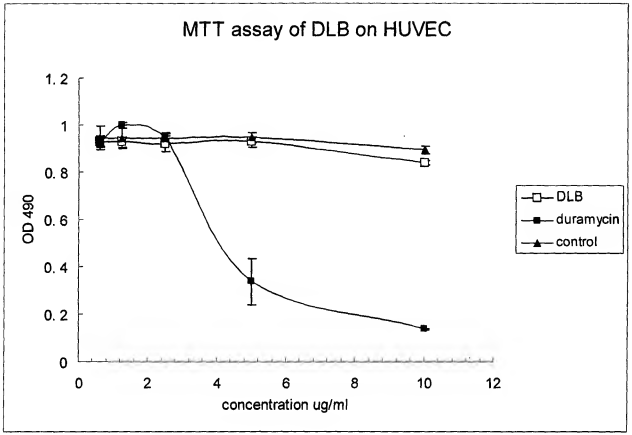

MTT assay of DLB on HUVEC
1.2
1
0.8
0.6
0.4
0.2
0
OD 490
0
2
4
6
8
10
12
concentration ug/ml
DLB
duramycin
control

FIG. 32

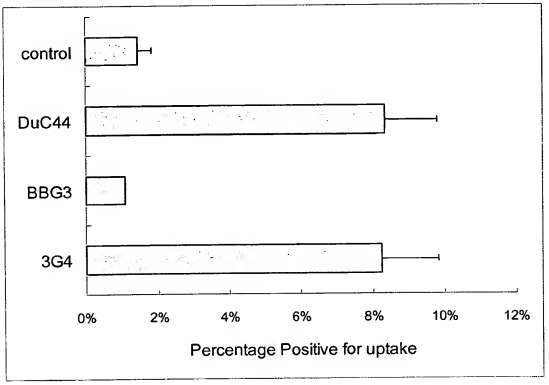

control
DuC44
BBG3
3G4
0%
2%
4%
6%
8%
10%
12%
Percentage Positive for uptake

FIG. 33